

413



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#2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,828

DATE: 04/03/2002

TIME: 16:10:38

Input Set : N:\Crf3\RULE60\10024828.raw

Output Set: N:\CRF3\04032002\J024828.raw

1 <110> APPLICANT: Virca, Duke
 2 Bird, Timothy A.
 3 Anderson, Dirk M.
 4 Marken, John S.
 5 <120> TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
 6 Functions
 7 <130> FILE REFERENCE: 2877-US
 8 <140> CURRENT APPLICATION NUMBER: 10/024,828
 9 <141> CURRENT FILING DATE: 2001-12-18
 11 <150> PRIOR APPLICATION NUMBER: US/09/509,902A
 12 <151> PRIOR FILING DATE: 1999-08-03
 15 <160> NUMBER OF SEQ ID NOS: 16
 16 <170> SOFTWARE: PatentIn Ver. 2.0
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 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
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 24 cacgcgcacc gagcgctcgg tgcctggagct ggtgcgccag gcgcccttcc tggtcacgct 120
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 29 <211> LENGTH: 221
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 32 <400> SEQUENCE: 2
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 35 ggctggagca cctgaaggag cacgggatca tccaccggga cctgtgcctg gagaacctgc 180
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 38 <210> SEQ ID NO: 3
 39 <211> LENGTH: 1085
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Homo sapiens
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 44 acctgctggt gccctggagg ctctgagccc cggcggcgcc cgggcccacg cggaacgacg 120
 45 gggcgagatg cgagccaccc ctctggctgc tccctgcgggt tccctgtcca ggaagaagcg 180
 46 gttggagttg gatgacaact tagataccga gcgtcccgtc cagaaacgag ctccaagtgg 240
 47 gccccagccc agactgcccc cctgcctggt gccctgagc ccacctactg ctccagatcg 300
 48 tgcaactgct gtggccactg cctcccgtct tgggccctat gtcctcctgg agcccagagga 360
 49 gggcggcgcg gcctaccagg ccctgcactg ccctacaggc actgagtata cctgcaaggt 420

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50      gtaccccgtc caggaagccc tggccgtgct ggagccctac gcgcggctgc ccccgacaaa 480
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52      tcggacccat ggggacatgc acagcctggt gcgaagccgc caccgtatcc ctgagcctga 600
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55      ggtgctggag aacctggagg actcctgctg gctgactggg ccagatgatt ccctgtggga 780
56      caagcacgcg tgcccagcct acgtgggacc tgagatactc agctcacggg cctcatactc 840
57      gggcaaggca gccgatgtct ggagcctggg cgtggcgctc ttcacatgc tggccggcca 900
58      ctaccccttc caggactcgg agcctgtcct gctcttcggc aagatccgcc gcggggccta 960
59      cgccttgctt gcaggcctct cggcccctgc ccgctgtctg gtctcgtgcc tccttcgtcg 1020
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65 <212> TYPE: DNA

66 <213> ORGANISM: Homo sapiens

67 <400> SEQUENCE: 4

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70      agaggtacgc tgtggaatga gatagaaagg ctgaaggaca aaggcaactt cctgaccgag 180
71      gatcaaatac tttggctgct gctggggatc tgcagaggcc ttgaggccat tcatgccaag 240
72      ggttatgcct acagagactt gaagcccacc aatatattgc ttggagatga ggggcagcca 300
73      gttttaatgg acttgggttc catgaatcaa gcatgcatcc atgtggaggg ctcccgccag 360
74      gctctgaccc tgcaggactg ggcagccc 388

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78 <212> TYPE: DNA

79 <213> ORGANISM: Homo sapiens

80 <400> SEQUENCE: 5

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83      aatttgaagc atattatcac ccttggccag gtcattccca aacggtgtga agagatgaaa 180
84      tactgcaaga aacagtgccg gcgcctgggc caccgcgtcc tcggcctgat caagcctctg 240
85      gagatgctcc aggaccaagg aaagaggagc gtgccctctg agaagttaac cacagccatg 300
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89      cctgtttcac ccataagcca aggagcgtcc tgggcacagg aagatcagca ggatgcagac 540
90      gaagacaggc gagctttcca gatgctaaga agagataatg aaaaaataga agcttactg 600
91      agacgattag aatcaacat gaaagaaatc aaggaaactt tgaggcagta tttaccacca 660
92      aatgcatgc aggagatccc gcaagagcaa atcaaggaga tcaagaagga gcagctttca 720
93      ggatccccgt ggattctgct aagggaatc gaagtcagca cactttataa aggagaatac 780
94      cacagagctc cagtggccat aaaagtattc aaaaaactcc aggttggcag cattgcaata 840
95      gtgaggcaga ctttcaataa ggagatcaaa accatgaaga aattcgaatc tcccaacatc 900
96      ctgcgtatat ttgggatttg cattgatgaa acagtgactc cgcctcaatt ctccattgtc 960
97      atggagtact gtgaactcgg gaccctgagg gagctgttgg atagggaaaa agacctcaca 1020
98      cttggcaagc gcatggctct agtcctgggg gcagcccag gcctataacc gctacaccat 1080
99      tcagaagcac ctgaactcca cggaaaaatc agaagctcaa acttctggt aactcaaggc 1140
100     taccaagtga agcttgcagg atttgagttg aggaaaacac agacttccat gagtttggga 1200

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101      actacgagag aaaagacaga cagagtcaaa tctacagcat atctctcacc tcaggaactg 1260
102      gaagatgtat tttatcaata tgatgtaaag tctgaaatat acagctttgg aatcgtcctc 1320
103      tgggaaatcg ccactggaga tatcccgttt caaggctgta attctgagaa gatccgcaag 1380
104      ctggtggctg tgaagcggca gcaggagcca ctgggtgaag actgcccttc agagctgcgg 1440
105      gagatcattg atgagtgccg ggcagcaggt cgtctcgttc caagatctgt agcggccgcc 1500
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115      catggagcag agcctccgtg cgggccccaa cgagcccagag ggcggcgaca agagccgcaa 180
116      aagcgccaag ggggacaaag gcggaaagga taaaaagcag attcagacct ctcccgttcc 240
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119      gaaggttaac cggaggctgc agctggagca agaaatggcc aaagctggac tctgtgaagc 420
120      tgagcaggag cagatgcgga agatcctcta ccagaaagag tctaattaca acaggttaaa 480
121      gagggccaag atggacaagt ctatgtttgt caagatcaaa accctgggga tcggtgcctt 540
122      tggagaagtg tgccttgctt gtaagggtga cactcacgcc ctgtacgcca tgaagaccct 600
123      aaggaaaaag gatgtcctga accggaatca ggtggcccac gtcaaggccg agagggacat 660
124      cctggccgag gcagacaatg agtgggtggt caaactctac tactccttcc aagacaaaga 720
125      cagcctgtac tttgtgatgg actacatccc tgggtggggac atgatgagcc tgctgatccg 780
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127      tgagagtgtc cacaagatgg gcttcatcca ccgagacatc aagcctgata acattttgat 900
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129      tcacaattcc aaatattacc agaaaggagg ccatgtcaga caggacagca tggagcccag 1020
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136      ggggcggaat ggggccgatg acctgaaggc ccacccttc ttcagcgcca ttgacttctc 1440
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140 <211> LENGTH: 60
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 7
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145          1             5             10             15
146      Thr Gln Glu His Thr Arg Thr Glu Arg Ser Val Leu Glu Leu Val Arg
147          20             25             30
148      Gln Ala Pro Phe Leu Val Thr Leu His Tyr Ala Phe Gln Thr Asp Ala
149          35             40             45
150      Lys Leu His Leu Ile Leu Asp Tyr Val Ser Gly Gly
151          50             55             60

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153 <210> SEQ ID NO: 8
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155 <212> TYPE: PRT
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160   Ala Ser His Gln Ala Glu Pro Glu Ala Tyr Glu Arg Arg Val Cys Phe
161               20             25             30
162   Leu Leu Leu Gln Leu Cys Asn Gly Leu Glu His Leu Lys Glu His Gly
163           35             40             45
164   Ile Ile His Arg Asp Leu Cys Leu Glu Asn Leu Leu Leu Val His Cys
165       50             55             60
166   Thr Leu Gln Ala Gly Pro Gly Pro Ala
167       65             70

169 <210> SEQ ID NO: 9
170 <211> LENGTH: 360
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
173 <400> SEQUENCE: 9
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176   Arg Ala Gly Pro Pro Ala Gly Ala Leu Glu Ala Leu Ser Pro Gly Gly
177               20             25             30
178   Ala Arg Ala His Ala Glu Arg Arg Gly Glu Met Arg Ala Thr Pro Leu
179           35             40             45
180   Ala Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu Glu Leu Asp
181       50             55             60
182   Asp Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala Arg Ser Gly
183       65             70             75             80
184   Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser Pro Pro Thr
185           85             90             95
186   Ala Pro Asp Arg Ala Thr Ala Val Ala Thr Ala Ser Arg Leu Gly Pro
187               100             105             110
188   Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly Arg Ala Tyr Gln Ala Leu
189           115             120             125
190   His Cys Pro Thr Gly Thr Glu Tyr Thr Cys Lys Val Tyr Pro Val Gln
191       130             135             140
192   Glu Ala Leu Ala Val Leu Glu Pro Tyr Ala Arg Leu Pro Pro His Lys
193       145             150             155             160
194   His Val Ala Arg Pro Thr Glu Val Leu Ala Gly Thr Gln Leu Leu Tyr
195           165             170             175
196   Ala Phe Phe Thr Arg Thr His Gly Asp Met His Ser Leu Val Arg Ser
197               180             185             190
198   Arg His Arg Ile Pro Glu Pro Glu Ala Ala Val Leu Phe Arg Gln Met
199           195             200             205
200   Ala Thr Ala Leu Ala His Cys His Gln His Gly Leu Val Leu Arg Asp
201       210             215             220
202   Leu Lys Leu Cys Arg Phe Val Phe Ala Asp Arg Glu Arg Lys Lys Leu

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203      225      230      235      240
204      Val Leu Glu Asn Leu Glu Asp Ser Cys Val Leu Thr Gly Pro Asp Asp
205      245      250      255
206      Ser Leu Trp Asp Lys His Ala Cys Pro Ala Tyr Val Gly Pro Glu Ile
207      260      265      270
208      Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys Ala Ala Asp Val Trp Ser
209      275      280      285
210      Leu Gly Val Ala Leu Phe Thr Met Leu Ala Gly His Tyr Pro Phe Gln
211      290      295      300
212      Asp Ser Glu Pro Val Leu Leu Phe Gly Lys Ile Arg Arg Gly Ala Tyr
213      305      310      315      320
214      Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala Arg Cys Leu Val Arg Cys
215      325      330      335
216      Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu Thr Ala Thr Gly Ile Leu
217      340      345      350
218      Leu His Pro Trp Leu Arg Gln Asp
219      355      360
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222 <211> LENGTH: 146
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224 <213> ORGANISM: Homo sapiens
225 <220> FEATURE:
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227 <222> LOCATION: (140)..(140)
228 <223> OTHER INFORMATION: UNSURE
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232      Arg Leu Val Ala Tyr Cys Leu Arg Glu Arg Gly Ala Lys His Glu Ala
233      20      25      30
234      Trp Leu Leu Leu Pro Phe Phe Lys Arg Gly Thr Leu Trp Asn Glu Ile
235      35      40      45
236      Glu Arg Leu Lys Asp Lys Gly Asn Phe Leu Thr Glu Asp Gln Ile Leu
237      50      55      60
238      Trp Leu Leu Leu Gly Ile Cys Arg Gly Leu Glu Ala Ile His Ala Lys
239      65      70      75      80
240      Gly Tyr Ala Tyr Arg Asp Leu Lys Pro Thr Asn Ile Leu Leu Gly Asp
241      85      90      95
242      Glu Gly Gln Pro Val Leu Met Asp Leu Gly Ser Met Asn Gln Ala Cys
243      100      105      110
244      Ile His Val Glu Gly Ser Arg Gln Ala Leu Thr Leu Gln Asp Trp Ala
245      115      120      125
W--> 246      Ala Gln Arg Cys Thr Ile Ser Tyr Arg Ala Pro Xaa Leu Phe Ser Val
247      130      135      140
248      Gln Ser
249      145
251 <210> SEQ ID NO: 11
252 <211> LENGTH: 505
253 <212> TYPE: PRT

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VERIFICATION SUMMARY

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L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10